

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: SAN FRANCISCO
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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) (B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: CGAB-210

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG

60

5 ACAACAAACC ATGGCTGCTG CTCCCAGTGT GAGGACGTTT ACTCGGGCCG AGGTTTTGAA 120
 TGCCGAGGCT CTGAATGAGG GCAAGAAGGA TGCCGAGGCA CCCTTCTTGA TGATCATCGA 180
 CAACAAGGTG TACGATGTCC GCGAGTTCGT CCCTGATCAT CCCGGTGGAA GTGTGATTCT 240
 CACGCACGTT GGCAAGGACG GCACTGACGT CTTTGACACT TTTCACCCCG AGGCTGCTTG 300
 10 GGAGACTCTT GCCAACTTTT ACGTTGGTGA TATTGACGAG AGCGACCGCG ATATCAAGAA 360
 TGATGACTTT GCGGCCGAGG TCCGCAAGCT GCGTACCTTG TTCCAGTCTC TTGGTTACTA 420
 CGATTCTTCC AAGGCATACT ACGCCTTCAA GGTCTCGTTC AACCTCTGCA TCTGGGGTTT 480
 15 GTCGACGGTC ATTGTGGCCA AGTGGGGCCA GACCTCGACC CTCGCCAACG TGCTCTCGGC 540
 TGCGCTTTTG GGTCTGTTCT GGCAGCAGTG CGGATGGTTG GCTCACGACT TTTTGCATCA 600
 20 CCAGGTCTTC CAGGACCGTT TCTGGGGTGA TCTTTTCGGC GCCTTCTTGG GAGGTGTCTG 660
 CCAGGGCTTC TCGTCCTCGT GGTGGAAGGA CAAGCACAACT ACTCACCACG CCGCCCCCAA 720
 CGTCCACGGC GAGGATCCCG ACATTGACAC CCACCCTCTG TTGACCTGGA GTGAGCATGC 780
 25 GTTGGAGATG TTCTCGGATG TCCCAGATGA GGAGCTGACC CGCATGTGGT CGCGTTTCAT 840
 GGTCTGAAC CAGACCTGGT TTTACTTCCC CATTCTCTCG TTTGCCCGTC TCTCTGGTG 900
 30 CCTCCAGTCC ATTCTCTTTG TGCTGCCTAA CGGTCAGGCC CACAAGCCCT CGGGCGCGCG 960
 TGTGCCATC TCGTTGGTCG AGCAGCTGTC GCTTGCATG CACTGGACCT GGTACCTCGC 1020
 CACCATGTTT CTGTTTCATCA AGGATCCCGT CAACATGCTG GTGTACTTTT TGTTGTGCGA 1080
 35 GGCGGTGTGC GGAAACTTGT TGGCGATCGT GTTCTCGCTC AACCACAACG GTATGCCTGT 1140
 GATCTCGAAG GAGGAGGCGG TCGATATGGA TTTCTTCACG AAGCAGATCA TCACGGGTCG 1200
 40 TGATGTCCAC CCGGGTCTAT TTGCCAACTG GTTACGGGT GGATTGAACT ATCAGATCGA 1260
 GCACCACTTG TTCCCTTCGA TGCCTCGCCA CAACTTTTCA AAGATCCAGC CTGCTGTGCA 1320
 GACCCTGTGC AAAAAGTACA ATGTCCGATA CCACACCACC GGTATGATCG AGGGAACCTG 1380
 45 AGAGGTCTTT AGCCGTCTGA ACGAGGTCTC CAAGGCTGCC TCCAAGATGG GTAAGGCGCA 1440
 GTAAAAAAA AAACAAGGAC GTTTTTTTTC GCCAGTGCCT GTGCCTGTGC CTGCTTCCCT 1500
 50 TGTCAAGTCG AGCGTTTCTG GAAAGGATCG TTCAGTGCAG TATCATCATT CTCCTTTTAC 1560
 CCCCCGCTCA TATCTCATTC ATTTCTCTTA TTAAACAACT TGTTCCCCC TTCACCG 1617

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 457 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
 1 5 10 15
 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
 20 25 30
 10 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
 35 40 45
 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
 50 55 60
 15 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
 65 70 75 80
 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
 85 90 95
 20 Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
 100 105 110
 25 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
 115 120 125
 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
 130 135 140
 30 Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
 145 150 155 160
 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
 165 170 175
 35 His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
 180 185 190
 40 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
 195 200 205
 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
 210 215 220
 45 Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
 225 230 235 240
 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
 245 250 255
 50 Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
 260 265 270
 55 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
 275 280 285
 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
 290 295 300
 60 Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
 305 310 315 320
 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
 325 330 335
 65 Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His

340 345 350
 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
 355 360 365
 5 Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
 370 375 380
 10 Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 385 390 395 400
 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
 405 410 415
 15 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
 420 425 430
 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
 435 440 445
 20 Ala Ala Ser Lys Met Gly Lys Ala Gln
 450 455

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 GTCCCCTGTC GCTGTGCGCA CACCCCATCC TCCCTCGCTC CCTCTGCGTT TGTCCCTTGGC 60
 CCACCGTCTC TCCTCCACCC TCCGAGACGA CTGCAACTGT AATCAGGAAC CGACAAATAC 120
 ACGATTTCTT TTTACTCAGC ACCAACTCAA AATCCTCAAC CGCAACCCTT TTTCAGGATG 180
 45 GCACCTCCCA AACTATCGA TGCCGGTTTG ACCCAGCGTC ATATCAGCAC CTCGGCCCCA 240
 AACTCGGCCA AGCCTGCCTT CGAGCGCAAC TACCAGCTCC CCGAGTTCAC CATCAAGGAG 300
 50 ATCCGAGAGT GCATCCCTGC CCACTGCTTT GAGCGCTCCG GTCTCCGTGG TCTCTGCCAC 360
 GTTGCCATCG ATCTGACTTG GGCCTCGCTC TTGTTCTTGG CTGCGACCCA GATCGACAAG 420
 TTTGAGAATC CCTTGATCCG CTATTTGGCC TGGCCTGTTT ACTGGATCAT GCAGGGTATT 480
 55 GTCTGCACCG GTGTCTGGGT GCTGGCTCAC GAGTGTGGTC ATCAGTCCTT CTCGACCTCC 540
 AAGACCCTCA ACAACACAGT TGTTTGGATC TTGCACTCGA TGCTCTTGGT CCCCTACCAC 600
 TCCTGGAGAA TCTCGCACTC GAAGCACCAC AAGGCCACTG GCCATATGAC CAAGGACCAG 660
 60 GTCTTTGTGC CCAAGACCCG CTCCCAGGTT GGCTTGCTC CCAAGGAGAA CGTGCTGTCT 720
 GCCGTTTCTG AGGAGGACAT GTCCGTGCAC CTGGATGAGG AGGCTCCCAT TGTGACTTTG 780
 65 TTCTGGATGG TGATCCAGTT CTTGTTTCGGA TGGCCCGCGT ACCTGATTAT GAACGCCTCT 840

5 GGCCAAGACT ACGGCCGCTG GACCTCGCAC TTCCACACGT ACTCGCCCAT CTTTGAGCCC 900
 CGCAACTTTT TCGACATTAT TATCTCGGAC CTCGGTGTGT TGGCTGCCCT CGGTGCCCTG 960
 ATCTATGCCT CCATGCAGTT GTCGCTCTTG ACCGTCACCA AGTACTATAT TGTCCCCTAC 1020
 CTCTTTGTCA ACTTTTGGTT GGTCTGATC ACCTTCTTGC AGCACACCGA TCCCAAGCTG 1080
 10 CCCCATTACC GCGAGGGTGC CTGGAATTTT CAGCGTGGAG CTCTTTGCAC CGTTGACCGC 1140
 TCGTTTGGCA AGTTCTTGGA CCATATGTTT CACGGCATTG TCCACACCCA TGTGGCCCAT 1200
 CACTTGTCTT CGCAAATGCC GTTCTACCAT GCTGAGGAAG CTACCTATCA TCTCAAGAAA 1260
 15 CTGCTGGGAG AGTACTATGT GTACGACCCA TCCCGATCG TCGTTGCGGT CTGGAGGTCG 1320
 TTCCGTGAGT GCCGATTCTG GGAGGATCAG GGAGACGTGG TCTTTTTCAA GAAGTAAAAA 1380
 AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC 1440
 20 CACTTCATAA AAGAACATGA GCTCTAGAGG CGTGTCAATC GCGCCTCC 1488

(2) INFORMATION FOR SEQ ID NO:4:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 30 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 35
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 40 Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
 1 5 10 15
 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
 20 25 30
 45 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
 35 40 45
 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
 50 55 60
 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
 65 70 75 80
 55 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
 85 90 95
 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
 100 105 110
 60 Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
 115 120 125
 Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
 130 135 140
 65 Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
 145 150 155 160

5 Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
 165 170 175
 10 Glu Asn Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
 180 185 190
 15 Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
 195 200 205
 20 Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
 210 215 220
 25 Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
 225 230 235 240
 30 Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
 245 250 255
 35 Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
 260 265 270
 40 Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
 275 280 285
 45 Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
 290 295 300
 50 Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
 305 310 315 320
 55 Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
 325 330 335
 60 Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
 340 345 350
 65 Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
 355 360 365
 70 Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
 370 375 380
 75 Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
 385 390 395

(2) INFORMATION FOR SEQ ID NO:5:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu Val Arg Lys Leu Arg Thr Leu Phe Gln Ser Leu Gly Tyr Tyr Asp
 1 5 10 15
 Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
 20 25 30

5 Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
 35 40 45
 10 Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
 50 55 60
 15 Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
 65 70 75 80
 20 Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
 85 90 95
 25 Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
 100 105 110
 30 Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
 115 120 125
 35 Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
 130 135 140
 40 Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
 145 150 155 160
 45 Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
 165 170 175
 50 Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
 180 185 190
 55 Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
 195 200 205
 60 His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
 210 215 220
 65 Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
 225 230 235 240
 70 Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
 245 250 255
 75 Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
 260 265 270
 80 Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
 275 280 285
 85 Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
 290 295 300
 90 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
 305 310 315 320
 95 Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
 325 330 335
 100 Val Phe Ser Arg Leu Asn Glu Val Ser Lys Ala Ala Ser Lys Met Gly
 340 345 350
 105 Lys Ala Gln
 355

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
 1 5 10 15
 Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
 20 25 30
 Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
 35 40 45
 Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
 50 55 60
 Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
 65 70 75 80
 Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
 85 90 95
 Gly Pro Asn Leu Gln His Ile Pro
 100

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln
 1 5 10 15
 Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile
 20 25 30
 Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn
 35 40 45
 Arg Phe Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ser Ile
 50 55 60
 Ala Trp Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser
 65 70 75 80
 Leu Asp Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser
 85 90 95

5 Thr Lys Phe Phe Ser Ser Leu Thr Ser Arg Phe Tyr Asp Arg Lys Leu
 100 105 110
 10 Thr Phe Gly Pro Val Ala Arg Phe Leu Val Ser Tyr Gln His Phe Thr
 115 120 125
 15 Tyr Tyr Pro Val Asn Cys Phe Gly Arg Ile Asn Leu Phe Ile Gln Thr
 130 135 140
 20 Phe Leu Leu Leu Phe Ser Lys Arg Glu Val Pro Asp Arg Ala Leu Asn
 145 150 155 160
 25 Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro Leu Leu Val Ser
 165 170 175
 30 Cys Leu Pro Asn Trp Pro Glu Arg Phe Phe Phe Val Phe Thr Ser Phe
 180 185 190
 35 Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu Asn His Phe Ala
 195 200 205
 40 Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp Trp Phe Glu Lys
 210 215 220
 45 Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser Tyr Met Asp Trp
 225 230 235 240
 50 Phe Phe Gly Gly Leu Gln Phe Gln Leu Glu His His
 245 250

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Xaa Xaa Asn Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro
 1 5 10 15
 Leu Leu Val Ser Cys Leu Pro Asn Trp Pro Glu Arg Phe Xaa Phe Val
 20 25 30
 Phe Thr Gly Phe Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu
 35 40 45
 Asn His Phe Ala Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp
 50 55 60
 Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
 65 70 75 80
 Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
 85 90 95
 Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
 100 105 110

Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
 115 120 125

5 (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Ala Thr Glu Val Gly Gly Leu Ala Trp Met Ile Thr Phe Tyr Val
 1 5 10 15
 Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
 20 25 30
 Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
 35 40 45
 Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
 50 55 60
 Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
 65 70 75 80
 Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
 85 90 95
 His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110
 Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125
 Lys Pro Leu
 130

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
 1 5 10 15
 Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 20 25 30

5 Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
 35 40 45
 Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
 50 55 60
 10 Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
 65 70 75 80
 Leu Val Gln Ala Lys Ala Ala
 85

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30 Arg His Glu Ala Ala Arg Gly Gly Thr Arg Leu Ala Tyr Met Leu Val
 1 5 10 15
 Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg
 20 25 30
 35 Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
 35 40 45
 40 Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
 50 55 60
 Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
 65 70 75 80
 45 Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
 85 90 95
 Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
 100 105 110
 50 His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
 115 120 125
 55 Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
 130 135 140

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 CCAAGCTTCT GCAGGAGCTC TTTTTTTTTT TTTT 35

(2) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG 33

(2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40 CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG 33

(2) INFORMATION FOR SEQ ID NO:15:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: other nucleic acid

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG 39

(2) INFORMATION FOR SEQ ID NO:16:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC

39

10 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

25 TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

40 AACTGATCTA GATTACTTCT TGAAAAAGAC CACGTCTCC

39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 nucleic acids

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: nucleic acid

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

55 CGTATGTCAC TCCATTCCAA ACTCGTTCAT GGTATCATAA ATATCAACAC ATTTACGCTC 60
CACTCCTCTA TGGTATTTAC AACTCTCAAAT ATCGTACTCA AGATTGGGAA GCTTTTGTA 120
AGGATGGTAA AAATGGTGCA ATTCGTGTTA GTGTCGCCAC AAATTCGAT AAGGCCGCTT 180
ACGTCATTGG TAAATTGTCT TTTGTTTTCT TCCGTTTCAT CCTTCCACTC CGTTATCATA 240
GCTTTACAGA TTTAATTTGT TATTTCTCTA TTGCTGAATT CGTCTTTGGT TGGTATCTCA 300
CAATTAATTT CCAAGTTAGT CATGTCGCTG AAGATCTCAA ATTCTTTGCT ACCCCTGAAA 360
GACCAGATGA ACCATCTCAA ATCAATGAAG ATTGGGCAAT CCTTCAACTT AAAACTACTC 420
AAGATTATGG TCATGGTTCA CTCCTTTGTA CCTTTTTTAG TGGTTCTTTA AATCATCAAG 480
TTGTTTCATCA TTTATTCCCA TCAATTGCTC AAGATTCTTA CCCACAATT GTACCAATTG 540
TAAAAGAAGT TTGTAAAGAA CATAACATTA CTTACCACAT TAAACCAAAC TTTACTGAAG 600
CTATTATGTC ACACATTAAT TACCTTTACA AAATGGGTAA TGATCCAGAT TATGTTAAAA 660
65 AACCATTAGC CTCAAAGAT GATTAAATGA AATAACTTAA AAACCAATTA TTTACTTTTG 720

ACAAACAGTA ATATTAATAA ATACAA

746

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln
 1 5 10 15
 His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr
 20 25 30
 Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly
 35 40 45
 Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr
 50 55 60
 Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro
 65 70 75
 Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile
 80 85 90
 Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val
 95 100 105
 Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
 110 115 120
 Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
 125 130 135
 Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
 140 145 150
 Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
 155 160 165
 Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
 170 175 180
 Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
 185 190 195
 Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
 200 205 210
 Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
 215 220 225
 Asp Asp ***

(2) INFORMATION FOR SEQ ID NO 21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 494 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTGGAAGG NTCCAAGTTN ACCACGGANT NGGCAAGTTN ACGGGGCGGA AANCGGTTTT 60
 CCCCCAAGC CTTTGTGCGA CTGGTTCTGT GGTGGCTTCC AGTACCAAGT CGACCACCAC 120
 TTATCCCCA GCCTGCCCGG ACACAATCTG GCCAAGACAC ACGCACTGGT CGAATCGTTC 180
 TGCAAGGAGT GGGGTGTCCA GTACCACGAA GCCGACCTCG TGGACGGGAC CATGGAAGTC 240
 TTGCACCATT TGGGCAGCGT GGCCGGCGAA TTCGTCGTGG ATTTTGTACG CGACGGACCC 300

GCCATGTAAT CGTCGTTCGT GACGATGCAA GGGTTCACGC ACATCTACAC ACACTCACTC 360
 ACACAACCTAG TGTAACCTCG ATAGAATTCG GTGTCGACCT GGACCTTGTT TGACTGGTTG 420
 GGGATAGGGT AGGTAGGCGG ACGCGTGGGT CGNCCCCGGG AATTCTGTGA CCGGTACCTG 480
 GCGCGCTNA AAGT 494

5

(2) INFORMATION FOR SEQ ID NO:22:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20

Phe Trp Lys Xxx Pro Ser Xxx Pro Arg Xxx Xxx Gln Val Xxx Gly
 1 5 10 15
 Ala Glu Xxx Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys
 20 25 30
 Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu
 25 35 40 45
 Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe
 50 55 60
 Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp
 65 70 75
 Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu
 80 85
 Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met

35

40

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 nucleic acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: nucleic acid

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTAAAGCGT CATGGGTGCG 60
 CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC 120
 ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG 180
 GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT 240
 GGTTCGTCAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCA 300
 CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC 360
 ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC 420
 TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC 480
 TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCTCCCGC 520

60

(2) INFORMATION FOR SEQ ID NO:24:

65

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

10

```

Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys
1      5      10      15
Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His
20      25      30
Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala
35      40      45
Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly
50      55      60
Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile
20      65      70      75
Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn
80      85      90
Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg
95      100      105
25      Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His
110      115      120
Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr
125      130      135
30      Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala
140      145      150
Lys Arg Asp
  
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35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: nucleic acid

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC      60
GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCCTTTTG      120
GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC      180
TCAGGGTCGC TCGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTCA CTGGTGTCAT      240
TTGGCTTGAC GACCGTTGT GCGAGTTCTT TTACGGCGTT GGTGTGGCA TGAGCGGTCA      300
TTACTGGAAA AACCAGCACA GCAAACACCA CGCAGCGCCA AACCGGCTCG AGCACGATGT      360
AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC      420
  
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55

(2) INFORMATION FOR SEQ ID NO:26:

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5 Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly
 1 5 10 15
 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu
 20 25 30
 10 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser
 35 40 45
 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser
 50 55 60
 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser
 65 70 75
 15 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe
 65 70 75
 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln
 80 85 90
 20 His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val
 95 100 105
 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val
 110 115 120
 Arg Lys Val Arg Pro
 125

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

40 GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA 60
 ACCTGATCCC AATTTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT 120
 45 TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCAATTTT GGGGCCTATG CGTTTGGCAG 180
 TTGCATTAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCCACAATG CTGCCTTTGG 240
 CAACTGCAAA GCAATGTGGA ATCGCTGGTT TGGAAATGTTT GCTAATCTTC CTATTGGGAT 300
 50 TCCATATTCA ATTTCTTTTA AGAGGTATCA CATGGATCAT CATCGGTACC TTGGAGCTGA 360
 TGGCGTCGAT GTAGATATTC CTACCGATTT TGAGGGCTGG TTCTTCTGTA CCGCTTTCAG 420
 55 AAAGTTTATA TGGGTTATTC TTCAGCCTCT CTTTTATGCC TTTCGACCTC TGTTTCATCA 480
 CCCCAAACCA ATTACGTATC TGGAAGTTAT CAATACCGTG GCACAGGTCA CTTTTGACAT 540
 TTTAATTTAT TACTTTTTGG GAATTAAATC CTTAGTCTAC ATGTTGGCAG CATCTTTACT 600
 60 TGGCCTGGGT TTGCACCCAA TTTCTGGACA TTTTATAGCT GAGCATTACA TGTTCTTAAA 660
 GGGTCATGAA ACTTACTCAT ATTATGGGCC TCTGAATTTA CTTACCTTCA ATGTGGGTTA 720
 TCATAATGAA CATCATGATT TCCCCAACAT TCCTGGAAAA AGTCTTCCAC TGGTGAGGAA 780
 65 AATAGCAGCT GAATACTATG ACAACCTCCC TCACTACAA TCCTGGATAA AAGTACTGTA 840

5 TGATTTTGTG ATGGATGATA CAATAAGTCC CTAACAAGA ATGAAGAGGC ACCAAAAAGG 900
 AGAGATGGTG CTGGAGTAAA TATCATTAGT GCCAAAGGGA TTCTTCTCCA AAACCTTAGA 960
 TGATAAAATG GAATTTTTCG ATTATTAAAC TTGAGACCAG TGATGCTCAG AAGCTCCCCT 1020
 GGCACAATTT CAGAGTAAGA GCTCGGTGAT ACCAAGAAGT GAATCTGGCT TTAAACAGT 1080
 10 CAGCCTGACT CTGTACTGCT CAGTTTCACT CACAGGAAAC TTGTGACTTG TGTATTATCG 1140
 TCATTGAGGA TGTTTCACTC ATGTCTGTCA TTTTATAAGC ATATCATTTA AAAAGCTTCT 1200
 15 AAAAAGCTAT TTCGCCAGG 1219

(2) INFORMATION FOR SEQ ID NO:28:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30 TTACCTTCTA CGTCCGCTTC TTCCTCACTT ATGTGCCACT ATTGGGGCTG AAAGCTTCCT 60
 GGGCCTTTTC TTCATAGTCA GGTTCTGGA AAGCAACTGG TTTGTGTGGG TGACACAGAT 120
 35 GAACCATATT CCCATGCACA TTGATCATGA CCGGAACATG GACTGGGTTT CCACCCAGCT 180
 CCAGGCCACA TGCAATGTCC ACAAGTCTGC CTTCAATGAC TGGTTCAGTG GACACCTCAA 240
 40 CTTCCAGATT GAGCACCATC TTTTCCAC GATGCCTCGA CACAATTACC ACAAAGTGGC 300
 TCCCCTGGTG CAGTCCTTGT GTGCCAAGCA TGGCATAGAG TACCAGTCCA AGCCCCTGCT 360
 GTCAGCCTTC GCCGACATCA TCCACTCACT AAAGGAGTCA GGGCAGCTCT GGCTAGATGC 420
 45 CTATCTTAC CAATAACAAC AGCCACCCTG CCCAGTCTGG AAGAAGAGGA GGAAGACTCT 480
 GGAGCCAAGG CAGAGGGGAG CTTGAGGGAC AATGCCACTA TAGTTTAATA CTCAGAGGGG 540
 50 GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA 600
 GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT 655

(2) INFORMATION FOR SEQ ID NO:29:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

65 GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTGT CCTTGCTACC 60

5 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
 CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
 AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
 10 CCCGATGTGA ACATGCTGCA CGTGTGTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
 AAGA 304

(2) INFORMATION FOR SEQ ID NO:30:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 918 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

25 CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 30 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 35 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC 420
 40 TTTGGGACGT CCTTTTGGCC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC 480
 CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG 540
 AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG 600
 45 AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC 660
 AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG 720
 50 AAGAAAAAAT ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA 780
 GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG 840
 TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC 900
 55 ACCGCAAATG CTTCTAAA 918

(2) INFORMATION FOR SEQ ID NO:31:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 65 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

5	GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA	60
	AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGGCG	120
10	AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAGC	180
	ACGAATACTT CTTCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTT CAGTACCAGA	240
	TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT	300
15	ACATCCGGTT CTTTCATCACC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTTCC	360
	TCAACTTCAT CAGGTTCTTG GAGAGCCACT GGTTTGTGTG GGTCACACAG ATGAATCACA	420
20	TCGTCATGGA GATTGACCAG GAGGCCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA	480
	CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGGACACCTT AACTTCCAGA	540
	TTGAGCACCA CCTCTTCCCC ACCATGCCCC GGCACAACCT ACACAAGATC GCCCCGCTGG	600
25	TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC	660
	TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC	720
30	ACAAATGAAG CCACAGCCCC CGGGACACCG TGGGAAGGG GTGCAGGTGG GGTGATGGCC	780
	AGAGGAATGA TGGGCTTTTG TTCTGAGGGG TGTCCGAGAG GCTGGTGTAT GCACTGCTCA	840
	CGGACCCCAT GTTGGATCTT TCTCCCTTTC TCCTCTCCTT TTTCTCTTCA CATCTCCCCC	900
35	ATAGCACCTT GCCCTCATGG GAQCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC	960
	TCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC	1020
40	TGTCCTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGAGA CCAGCGGTCC ATGGGTCTGG	1080
	CCTGTGAGTC TCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCCTTTG GTTCTTCAGA	1140
	TGCTCTTGGG GTTCATAGGG GCAGGTCCTA GTCGGGCAGG GCCCCTGACC CTCCCGGCTC	1200
45	GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCTTT CATAGAGAGG CCTGCTTTGT	1260
	TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTTAAGTAC CCGAGGCCTC TCTTAAGATG	1320
50	TCCAGGGCCC CAGGCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC	1380
	CACCCCATCA CTAGAGTGCT CTGACCCTGG GCTTTACAGG GCCCCATTCC ACCGCCTCCC	1440
	CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGA CTGAGCA	1500
55	GAGGCAGTGG CCACGTTTCA GAGGGGGCCG GCTGGCCTGG AGGCTCAGCC CACCCTCCAG	1560
	CTTTTCTCTCA GGGTGTCTTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCT TCTCCAAAGG	1620
60	CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG	1680
	GCCCTG	1686

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid (Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

10

GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60

TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120

15

CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180

AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240

20

CCCGATGTGA ACATGCTGCA CGTGTGTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300

AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG 360

CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT 420

25

AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTTCTT CATCACCTAC 480

ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTTCTCA ACTTCATCAG GTTCCTGGAG 540

30

AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG 600

GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC 660

TTCAACGACT GGTTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC 720

35

ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT 780

GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG 840

40

AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG 900

GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTC 960

TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCATGTT GGATCTTTCT 1020

45

CCCTTTCTCC TCTCCTTTTT CTCTTCACAT CTCCCCATA GCACCCTGCC CTCATGGGAC 1080

CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCCTTC 1140

50

TTCCAAGGAG CAGAGAGGTG GCCACCGGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC 1200

CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CTTGCAGCC 1260

TGGTCACTAG GCATCACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA 1320

55

GGTCCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG 1380

CCATTGGTCC ACCCTTTCAT AGAGAGGCCT GCTTTGTAC AAAGCTCGGG TCTCCCTCCT 1440

60

GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCGCGGGC 1500

ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCCTCCAC CCCATCACTA GAGTGCTCTG 1560

ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG 1620

65

ACCAAAGGGG GAGTCCCTCG TCTCTTGTA CTCAGCAGAG GCAGTGCCA CGTTCAGGGA 1680

GGGGCCGGCT GGCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCTCAGGG TGTCTGAGG 1740
 TCCAAGATTC TGGAGCAATC TGACCCTTCT CCAAAGGCTC TGTTATCAGC TGGGCAGTGC 1800
 5 CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG 1843

(2) INFORMATION FOR SEQ ID NO:33:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

20 CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 25 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 30 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGACG CCTGGCTCAC CCTTTGGGTC 420
 TTTGGGACGT CCTTTTTGCC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGCAG 480
 35 GCCCAAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG 540
 TGGAACCACC TTGTCCACAA ATTCGTCATT GGCCACTTAA AGGGTGCCTC TGCCAACCTGG 600
 40 TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCCACAA GGATCCCGAT 660
 GTGAACATGC TGCACGTGTT TGTCTGGGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG 720
 AAGCTGAAAT ACCTGCCCTA CAATCACCAG CACGAATACT TCTTCTGAT TGGGCCGCCG 780
 45 CTGCTCATCC CCATGTATTT CCAGTACCAG ATCATCATGA CCATGATCGT CCATAAGAAC 840
 TGGGTGGACC TGGCCTGGGC CGTCAGCTAC TACATCCGGT TCTTCATCAC CTACATCCCT 900
 50 TTCTACGGCA TCCTGGGAGC CCTCCTTTTC CTCAACTTCA TCAGGTTCCCT GGAGAGCCAC 960
 TGGTTTGTGT GGGTCACACA GATGAATCAC ATCGTCATGG AGATTGACCA GGAGGCCTAC 1020
 55 CGTGACTGGT TCAGTAGCCA GCTGACAGCC ACCTGCAACG TGGAGCAGTC CTTCTTCAAC 1080
 GACTGGTTCA GTGGACACCT TAACTTCCAG ATTGAGCACC ACCTCTTCCC CACCATGCCC 1140
 CGGCACAACT TACACAAGAT CGCCCCGCTG GTGAAGTCTC TATGTGCCAA GCATGGCATT 1200
 60 GAATACCAGG AGAAGCCGCT ACTGAGGGCC CTGCTGGACA TCATCAGGTC CCTGAAGAAG 1260
 TCTGGGAAGC TGTGGCTGGA CGCCTACCTT CACAAATGAA GCCACAGCCC CCGGGACACC 1320
 65 GTGGGGAAGG GGTGCAGGTG GGGTGATGGC CAGAGGAATG ATGGGCTTTT GTTCTGAGGG 1380
 GTGTCCGAGA GGCTGGTGTA TGCACTGCTC ACGGACCCCA TGTGGATCT TTCTCCCTTT 1440

CTCCTCTCCT TTTTCTCTTC ACATCTCCCC CATAGCACCC TGCCCTCATG GGACCTGCCC 1500
 5 TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCTAGCCC CTTCTTCCAA 1560
 GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGTCTTACC TCCACTCTCT GCCCCTAAAG 1620
 ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA 1680
 10 CTAGGCATCA CCCCCGCTTT GGTCTTTCAG ATGCTCTTGG GGTTCATAGG GGCAGGTCCT 1740
 AGTCGGGCAG GGGCCCTGAC CCTCCCGGCC TGGCTTCACT CTCCCTGACG GCTGCCATTG 1800
 15 GTCCACCCTT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT 1860
 CGGTAAAGTA CCCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCCG GGGCACAGCC 1920
 AGCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCCTG 1980
 20 GGCTTTCACG GGGCCCATTC CACCGCTCC CCAACTTGAG CCTGTGACCT TGGGACCAAA 2040
 GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGGCC 2100
 25 GGCTGGCCTG GAGGCTCAGC CCACCCTCCA GCTTTTCCTC AGGGTGTCTT GAGGTCCAAG 2160
 ATTCTGGAGC AATCTGACCC TTCTCAAAG GCTCTGTTAT CAGCTGGGCA GTGCCAGCCA 2220
 ATCCCTGGCC ATTGGCCCC AGGGGACGTG GGCCCTG 2257

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

45 His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile
 1 5 10 15
 Lys Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile
 20 25 30
 Met Met Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp
 35 40 45
 50 Leu Asp Trp Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser
 50 55 60
 Cys Ile Asn His Ser Met Thr Leu Ala Ile His Glu Ile Ala His
 65 70 75
 55 Asn Ala Ala Phe Gly Asn Cys Lys Ala Met Trp Asn Arg Trp Phe
 80 85 90
 Gly Met Phe Ala Asn Leu Pro Ile Gly Ile Pro Tyr Ser Ile Ser
 95 100 105
 Phe Lys Arg Tyr His Met Asp His His Arg Tyr Leu Gly Ala Asp
 110 115 120
 60 Gly Val Asp Val Asp Ile Pro Thr Asp Phe Glu Gly Trp Phe Phe
 125 130 135
 Cys Thr Ala Phe Arg Lys Phe Ile Trp Val Ile Leu Gln Pro Leu
 140 145 150
 65 Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn Pro Lys Pro Ile Thr
 155 160 165
 Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val Thr Phe Asp Ile

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Leu Ile Tyr Tyr	170	175	180
Phe Leu Gly Ile Lys Ser Leu Val Tyr Met Leu	185	190	195
Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser Gly His	200	205	210
Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr Tyr	215	220	225
Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr	230	235	240
His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu	245	250	255
Pro Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro	260	265	270
His Tyr Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp	275	280	285
Asp Thr Ile Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly	290	295	300
Glu Met Val Leu Glu *** Ile Ser Leu Val Pro Lys Gly Phe Phe	305	310	315
Ser Lys Thr Leu Asp Asp Lys Met Glu Phe Leu His Tyr *** Thr	320	325	330
*** Asp Gln *** Cys Ser Glu Ala Pro Leu Ala Gln Phe Gln Ser	335	340	345
Lys Ser Ser Val Ile Pro Arg Ser Glu Ser Gly Phe *** Thr Val	350	355	360
Ser Leu Thr Leu Tyr Cys Ser Val Ser Leu Thr Gly Asn Leu ***	365	370	375
Leu Val Tyr Tyr Arg His *** Gly Cys Phe Thr His Val Cys His	380	385	390
Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu Lys Ser Tyr Phe Ala	400	405	410
Arg			

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly	1	5	10	15
Ala Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu	20	25	30	35
Ser Asn Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met	40	45	50	55
His Ile Asp His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu	60	65	70	75
Gln Ala Thr Cys Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe	80	85	90	95
Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr	100	105	110	115
Met Pro Arg His Asn Tyr His Lys Val Ala Pro Leu Val Gln Ser	120	125	130	135
Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser Lys Pro Leu Leu	140	145	150	155
Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu S r Gly Gln	160	165	170	175
Leu Trp Leu Asp Ala Tyr Leu His Gln *** Gln Gln Pro Pro Cys	180	185	190	195

5 Pro Val Trp Lys Lys Arg Arg Lys Thr Leu Glu Pro Arg Gln Arg
 155 160 165
 Gly Ala *** Gly Thr Met Pro Leu *** Phe Asn Thr Gln Arg Gly
 170 175 180
 10 Leu Gly Leu Gly Thr *** Ser Leu *** Leu Lys Leu Leu Pro Phe
 185 190 195
 Ile Phe *** Pro Gln Phe *** Asp Pro Lys Trp Gly Val Asp Thr
 200 205 210
 15 Glu Val Pro Arg Arg Glu Gly Ala
 215

15 (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

30 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
 1 5 10 15
 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
 20 25 30
 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
 35 35 40 45
 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
 50 55 60
 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
 65 70 75
 40 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xxx
 80 85

45 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 amino acids
 (B) TYPE: amino acid
 50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

60 Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
 1 5 10 15
 Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
 20 25 30
 Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
 35 40 45
 Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
 50 55 60
 65 Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
 65 70 75
 Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro

5 80 85 90
 Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
 95 100 105
 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
 110 115 120
 Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
 125 130 135
 Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
 140 145 150
 10 Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu
 155 160 165
 Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
 170 175 180
 15 Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala
 185 190 195
 Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys
 200 205 210
 Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe
 215 220 225
 20 Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
 230 235 240
 Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xxx Tyr Phe Phe
 245 250 255
 25 Leu Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr
 260 265 270
 Ile Phe Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala
 275 280 285
 Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser
 290 295 300
 30 Thr Ala Asn Ala Ser Lys
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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

50 5 10 15
 His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe
 1 20 25 30
 Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val
 35 40 45
 Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu
 50 55 60
 Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His
 55 Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
 65 70 75
 Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp
 80 85 90
 Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile
 95 100 105
 60 Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu
 110 115 120
 Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr
 125 130 135
 65 Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg
 140 145 150

Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
 155 160 165
 Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile
 170 175 180
 Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys
 185 190 195
 Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu
 200 205 210
 Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
 215 220 225
 Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His
 230 235 240
 Lys *** Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg
 245 250 255
 Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe *** Gly Val
 260 265 270
 Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp
 275 280 285
 Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His
 290 295 300
 Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro
 305 310 315
 Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly
 320 325 330
 Ala Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser
 335 340 345
 Leu Pro Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala
 350 355 360
 Cys Glu Ser Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala
 365 370 375
 Leu Val Leu Gln Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser
 380 385 390
 Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu His Ser Pro ***
 400 405 410
 Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro Ala Leu Leu
 415 420 425
 Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg Gly
 430 435 440
 Leu Ser *** Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser
 445 450 455
 Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His *** Ser
 460 465 470
 Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
 475 480 485
 Thr *** Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu
 490 495 500
 Leu *** Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly
 505 510 515
 Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val
 520 525 530
 Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala
 535 540 545
 Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
 550 555 560
 Pro Gly Asp Val Gly Pro Xxx
 565

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 619 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

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Val	Phe	Tyr	Phe	Gly	Asn	Gly	Trp	Ile	Pro	Thr	Leu	Ile	Thr	Ala
1				5					10					15
Phe	Val	Leu	Ala	Thr	Ser	Gln	Ala	Gln	Ala	Gly	Trp	Leu	Gln	His
				20					25					30
Asp	Tyr	Gly	His	Leu	Ser	Val	Tyr	Arg	Lys	Pro	Lys	Trp	Asn	His
				35					40					45
Leu	Val	His	Lys	Phe	Val	Ile	Gly	His	Leu	Lys	Gly	Ala	Ser	Ala
				50					55					60
Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln	His	His	Ala	Lys	Pro	Asn
				65					70					75
Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	His	Val	Phe	Val
				80					85					90
Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	Lys	Leu	Lys
				95					100					105
Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	Leu	Ile	Gly
				110					115					120
Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln	Ile	Ile	Met
				125					130					135
Thr	Met	Ile	Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala	Trp	Ala	Val
				140					145					150
Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly
				155					160					165
Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg	Phe	Leu	Glu
				170					175					180
Ser	His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	Ile	Val	Met
				185					190					195
Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser	Ser	Gln	Leu
				200					205					210
Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn	Asp	Trp	Phe
				215					220					225
Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr
				230					235					240
Met	Pro	Arg	His	Asn	Leu	His	Lys	Ile	Ala	Pro	Leu	Val	Lys	Ser
				245					250					255
Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	Tyr	Gln	Glu	Lys	Pro	Leu	Leu
				260					265					270
Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	Ser	Leu	Lys	Lys	Ser	Gly	Lys
				275					280					285
Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Lys	***	Ser	His	Ser	Pro	Arg
				290					295					300
Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp	Gly	Asp	Gly	Gln	Arg	Asn
				305					310					315
Asp	Gly	Leu	Leu	Phe	***	Gly	Val	Ser	Glu	Arg	Leu	Val	Tyr	Ala
				320					325					330
Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro	Phe	Leu	Leu	Ser
				335					340					345
Phe	Phe	Ser	Ser	His	Leu	Pro	His	Ser	Thr	Leu	Pro	Ser	Trp	Asp
				350					355					360
Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro	Ser	Ala	Met	Ala	Leu	Pro	Val
				365					370					375
Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly	Ala	Glu	Arg	Trp	Pro	Pro	Gly
				380					385					390
Val	Ala	Leu	Ser	Tyr	Leu	His	Ser	Leu	Pro	Leu	Lys	Met	Gly	Gly
				400					405					410
Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala	Cys	Glu	Ser	Pro	Leu	Ala	Ala
				415					420					425
Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala	Leu	Val	Leu	Gln	Met	Leu	Leu
				430					435					440
Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser	Arg	Ala	Gly	Pro	Leu	Thr	Leu
				445					450					455

5 Pro Ala Trp Leu His Ser Pro *** Arg Leu Pro Leu Val His Pro
 460 465 470
 Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
 475 480 485
 10 Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser *** Asp Val Gln Gly
 490 495 500
 Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys
 505 510 515
 Ser Pro Pro Pro His His *** Ser Ala Leu Thr Leu Gly Phe His
 520 525 530
 Gly Pro His Ser Thr Ala Ser Pro Thr *** Ala Cys Asp Leu Gly
 535 540 545
 Thr Lys Gly Gly Val Pro Arg Leu Leu *** Leu Ser Arg Gly Ser
 550 555 560
 15 Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly Ser Ala His
 565 570 575
 Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys Ile Leu Glu
 580 585 590
 20 Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly Gln Cys
 595 600 605
 Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro Xxx
 610 615 620

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

40 Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
 1 5 10 15
 Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
 20 25 30
 Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
 35 40 45
 45 Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
 50 55 60
 Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
 65 70 75
 50 Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
 80 85 90
 Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
 95 100 105
 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
 110 115 120
 55 Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
 125 130 135
 Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
 140 145 150
 60 Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp
 155 160 165
 Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys
 170 175 180
 Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly
 185 190 195
 65 Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala
 200 205 210

	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	His	215	220	225
	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	230	235	240
5	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	245	250	255
	Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln	260	265	270
10	Ile	Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala	275	280	285
	Trp	Ala	Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	290	295	300
	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg	305	310	315
15	Phe	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	320	325	330
	Ile	Val	Met	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser	335	340	345
20	Ser	Gln	Leu	Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn	350	355	360
	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	365	370	375
	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	His	Lys	Ile	Ala	Pro	Leu	380	385	390
25	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	Tyr	Gln	Glu	Lys	400	405	410
	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	Ser	Leu	Lys	Lys	415	420	425
30	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Lys	***	Ser	His	430	435	440
	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp	Gly	Asp	Gly	445	450	455
	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	***	Gly	Val	Ser	Glu	Arg	Leu	460	465	470
35	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro	Phe	475	480	485
	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His	Leu	Pro	His	Ser	Thr	Leu	Pro	490	495	500
40	Ser	Trp	Asp	Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro	Ser	Ala	Met	Ala	505	510	515
	Leu	Pro	Val	Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly	Ala	Glu	Arg	Trp	520	525	530
	Pro	Pro	Gly	Val	Ala	Leu	Ser	Tyr	Leu	His	Ser	Leu	Pro	Leu	Lys	535	540	545
45	Met	Gly	Gly	Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala	Cys	Glu	Ser	Pro	550	555	560
	Leu	Ala	Ala	Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala	Leu	Val	Leu	Gln	565	570	575
50	Met	Leu	Leu	Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser	Arg	Ala	Gly	Pro	580	585	590
	Leu	Thr	Leu	Pro	Ala	Trp	Leu	His	Ser	Pro	***	Arg	Leu	Pro	Leu	595	600	605
	Val	His	Pro	Phe	Ile	Glu	Arg	Pro	Ala	Leu	Leu	Gln	Ser	Ser	Gly	610	615	620
55	Leu	Pro	Pro	Ala	Ala	Arg	Leu	Ser	Thr	Arg	Gly	Leu	Ser	***	Asp	625	630	635
	Val	Gln	Gly	Pro	Arg	Pro	Ala	Gly	Thr	Ala	Ser	Pro	Asn	Leu	Gly	640	645	650
60	Pro	Trp	Lys	Ser	Pro	Pro	Pro	His	His	***	Ser	Ala	Leu	Thr	Leu	655	660	665
	Gly	Phe	His	Gly	Pro	His	Ser	Thr	Ala	Ser	Pro	Thr	***	Ala	Cys	670	675	680
	Asp	Leu	Gly	Thr	Lys	Gly	Gly	Val	Pro	Arg	Leu	Leu	***	Leu	Ser	685	690	695
65	Arg	Gly	Ser	Gly	His	Val	Gln	Gly	Gly	Ala	Gly	Trp	Pro	Gly	Gly	700	705	710

5 Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys
715 720 725
Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala
730 735 740
Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val
745 750 755
Gly Pro Xxx

SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION:
- 10 (i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA
- 15 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
- (iii) NUMBER OF SEQUENCES: 40
- 20 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LIMBACH AND LIMBACH LLP
(B) STREET: 2001 FERRY BUILDING
(C) CITY: SAN FRANCISCO
(D) STATE: CA
(E) COUNTRY: USA
25 (F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
30 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
35 (B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: WARD, MICHAEL R.
(B) REGISTRATION NUMBER: 38,651
(C) REFERENCE/DOCKET NUMBER: CGAB-210
- (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (415) 433-4150
(B) TELEFAX: (415) 433-8716
(C) TELEX: N/A
- 50 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG 60
 ACAACAAACC ATGGCTGCTG CTCCCAGTGT GAGGACGTTT ACTCGGGCCG AGGTTTTGAA 120
 TGCCGAGGCT CTGAATGAGG GCAAGAAGGA TGCCGAGGCA CCCTTCTTGA TGATCATCGA 180
 CAACAAGGTG TACGATGTCC GCGAGTTCGT CCCTGATCAT CCCGGTGGAA GTGTGATTCT 240
 10 CACGCACGTT GGCAAGGACG GCACTGACGT CTTTGACACT TTTCACCCCG AGGCTGCTTG 300
 GGAGACTCTT GCCAACTTTT ACGTTGGTGA TATTGACGAG AGCGACCGCG ATATCAAGAA 360
 TGATGACTTT GCGGCCGAGG TCCGCAAGCT GCGTACCTTG TTCCAGTCTC TTGGTTACTA 420
 15 CGATTCTTCC AAGGCATACT ACGCCTTCAA GGTCTCGTTC AACCTCTGCA TCTGGGGTTT 480
 GTCGACGGTC ATTGTGGCCA AGTGGGGCCA GACCTCGACC CTCGCCAACG TGCTCTCGGC 540
 TGCGCTTTTG GGTCTGTTCT GGCAGCAGTG CGGATGGTTG GCTCACGACT TTTTGCATCA 600
 20 CCAGGTCTTC CAGGACCGTT TCTGGGGTGA TCTTTTCGGC GCCTTCTTGG GAGGTGTCTG 660
 CCAGGGCTTC TCGTCCTCGT GGTGGAAGGA CAAGCACAAAC ACTCACCACG CCGCCCCCAA 720
 25 CGTCCACGGC GAGGATCCCG ACATTGACAC CCACCCTCTG TTGACCTGGA GTGAGCATGC 780
 GTTGAGATG TTCTCGGATG TCCCAGATGA GGAGCTGACC CGCATGTGGT CGCGTTTCAT 840
 GGTCTGAAC CAGACCTGGT TTTACTTCCC CATCTCTCG TTTGCCCCGTC TCTCCTGGTG 900
 30 CCTCCAGTCC ATTCTCTTTC TGCTGCCTAA CGGTCAGGCC CACAAGCCCT CGGGCGCGCG 960
 TGTGCCCATC TCGTTGGTCG AGCAGCTGTC GCTTGCGATG CACTGGACCT GGTACCTCGC 1020
 35 CACCATGTTC CTGTTTCATCA AGGATCCCGT CAACATGCTG GTGTACTTTT TGGTGTGCGA 1080
 GGCGGTGTGC GGAAACTTGT TGGCGATCGT GTTCTCGCTC AACCACAACG GTATGCCTGT 1140
 GATCTCGAAG GAGGAGGCGG TCGATATGGA TTTCTTCACG AAGCAGATCA TCACGGGTCG 1200
 40 TGATGTCCAC CCGGTCTAT TTGCCAACTG GTTCACGGGT GGATTGAACT ATCAGATCGA 1260
 GCACCACTTG TTCCCTTCGA TGCCTCGCCA CAACTTTTCA AAGATCCAGC CTGCTGTCGA 1320
 45 GACCCTGTGC AAAAAGTACA ATGTCCGATA CCACACCACC GGTATGATCG AGGGAACGTC 1380
 AGAGGTCTTT AGCCGTCTGA ACGAGGTCTC CAAGGCTGCC TCCAAGATGG GTAAGGCGCA 1440
 GTAAAAA AAAACAAGGAC GTTTTTTTTC GCCAGTGCCT GTGCCTGTGC CTGCTTCCCT 1500
 50 TGTCAAGTCG AGCGTTTCTG GAAAGGATCG TTCAGTGCAG TATCATCATT CTCCTTTTAC 1560
 CCCCCGCTCA TATCTCATTC ATTTCTCTTA TTAAACAAC TGTTCCCCCC TTCACCG 1617

55 (2) INFORMATION FOR SEQ ID NO:2:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 amino acids
 (B) TYPE: amino acid
 60 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
1 . 5 10 15

Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
20 25 30

10 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
35 40 45

15 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
50 55 60

Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
65 70 75 80

20 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85 90 95

Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
100 105 110

25 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
115 120 125

30 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
130 135 140

Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
145 150 155 160

35 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
165 170 175

His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
180 185 190

40 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
195 200 205

His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
210 215 220

Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
225 230 235 240

50 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
245 250 255

Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
260 265 270

55 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
275 280 285

Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
290 295 300

Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
305 310 315 320

65 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser

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SUBSTITUTE SHEET

	325	330	335
5	Gln Ala Val Cys Gly Asn Leu Leu	Ala Ile Val Phe Ser Leu Asn His	
	340	345	350
	Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe		
	355	360	365
10	Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe		
	370	375	380
	Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu		
	385	390	395
15	Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val		
	405	410	415
	Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met		
	420	425	430
20	Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys		
	435	440	445
	Ala Ala Ser Lys Met Gly Lys Ala Gln		
25	450	455	
	(2) INFORMATION FOR SEQ ID NO:3:		
30	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 1488 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
35	(ii) MOLECULE TYPE: DNA (genomic)		
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:		
	GTCCCTGTC GCTGTCGGCA CACCCATCC TCCCTCGCTC CCTCTGCGTT TGTCTTGGC	60	
45	CCACCGTCTC TCCTCCACCC TCCGAGACGA CTGCAACTGT AATCAGGAAC CGACAAATAC	120	
	ACGATTTCTT TTTACTCAGC ACCAACTCAA AATCCTCAAC CGCAACCCTT TTTCAGGATG	180	
	GCACCTCCCA ACACTATCGA TGCCGGTTTG ACCCAGCGTC ATATCAGCAC CTCGGCCCCA	240	
50	AACTCGGCCA AGCCTGCCTT CGAGCGCAAC TACCAGCTCC CCGAGTTCAC CATCAAGGAG	300	
	ATCCGAGAGT GCATCCCTGC CCACTGCTTT GAGCGCTCCG GTCTCCGTGG TCTCTGCCAC	360	
55	GTTGCCATCG ATCTGACTTG GGCCTCGCTC TTGTTCTTGG CTGCGACCCA GATCGACAAG	420	
	TTTGAGAATC CCTTGATCCG CTATTTGGCC TGGCCTGTTT ACTGGATCAT GCAGGGTATT	480	
	GTCTGCACCG GTGTCTGGGT GCTGGCTCAC GAGTGTGGTC ATCAGTCCTT CTCGACCTCC	540	
60	AAGACCCTCA ACAACACAGT TGGTTGGATC TTGCACTCGA TGCTCTTGGT CCCCTACCAC	600	
	TCCTGGAGAA TCTCGCACTC GAAGCACCAC AAGGCCACTG GCCATATGAC CAAGGACCAG	660	
65	GTCTTTGTGC CCAAGACCCG CTCCCAGGTT GGCTTGCCTC CCAAGGAGAA CGCTGCTGCT	720	

GCCGTTCAGG AGGAGGACAT GTCCGTGCAC CTGGATGAGG AGGCTCCCAT TGTGACTTTG 780
 TTCTGGATGG TGATCCAGTT CTTGTTCCGA TGGCCCGCGT ACCTGATTAT GAACGCCTCT 840
 5 GGCCAAGACT ACGGCCGCTG GACCTCGCAC TTCCACACGT ACTCGCCCAT CTTTGAGCCC 900
 CGCAACTTTT TCGACATTAT TATCTCGGAC CTCGGTGTGT TGGCTGCCCT CGGTGCCCTG 960
 10 ATCTATGCCT CCATGCAGTT GTCGCTCTTG ACCGTCACCA AGTACTATAT TGTCCCCTAC 1020
 CTCTTTGTCA ACTTTTGGTT GGTCTGATC ACCTTCTTGC AGCACACCGA TCCCAAGCTG 1080
 CCCCATTACC GCGAGGGTGC CTGGAATTC CAGCGTGGAG CTCTTTGCAC CGTTGACCGC 1140
 15 TCGTTTGGCA AGTTCTTGA CCATATGTT CACGGCATTG TCCACACCCA TGTGGCCCAT 1200
 CACTTGTCT CGCAAATGCC GTTCTACCAT GCTGAGGAAG CTACCTATCA TCTCAAGAAA 1260
 20 CTGCTGGGAG AGTACTATGT GTACGACCCA TCCCCGATCG TCGTTGCGGT CTGGAGGTCG 1320
 TTCCGTGAGT GCCGATTCGT GGAGGATCAG GGAGACGTGG TCTTTTCAA GAAGTAAAAA 1380
 AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC 1440
 25 CACTTCATAA AAGAACATGA GCTCTAGAG CGTGTCATTC GCGCCTCC 1488

(2) INFORMATION FOR SEQ ID NO:4:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
 1 5 10 15
 45 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
 20 25 30
 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
 35 40 45
 50 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
 50 55 60
 55 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
 65 70 75 80
 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
 85 90 95
 60 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
 100 105 110
 Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
 115 120 125
 65

	Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
	130 135 140
5	Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
	145 150 155 160
	Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
	165 170 175
10	Glu Asn Ala Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
	180 185 190
	Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
	195 200 205
15	Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
	210 215 220
	Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
	225 230 235 240
	Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
	245 250 255
25	Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
	260 265 270
	Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
	275 280 285
30	Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
	290 295 300
	Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
	305 310 315 320
35	Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
	325 330 335
40	Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
	340 345 350
	Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
	355 360 365
45	Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
	370 375 380
50	Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
	385 390 395

(2) INFORMATION FOR SEQ ID NO:5:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: peptide

- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Glu	Val	Arg	Lys	Leu	Arg	Thr	Leu	Phe	Gln	Ser	Leu	Gly	Tyr	Tyr	Asp	
	1				5					10					15		
5	Ser	Ser	Lys	Ala	Tyr	Tyr	Ala	Phe	Lys	Val	Ser	Phe	Asn	Leu	Cys	Ile	
				20					25					30			
	Trp	Gly	Leu	Ser	Thr	Val	Ile	Val	Ala	Lys	Trp	Gly	Gln	Thr	Ser	Thr	
			35					40					45				
10	Leu	Ala	Asn	Val	Leu	Ser	Ala	Ala	Leu	Leu	Gly	Leu	Phe	Trp	Gln	Gln	
		50					55					60					
	Cys	Gly	Trp	Leu	Ala	His	Asp	Phe	Leu	His	His	Gln	Val	Phe	Gln	Asp	
15	65					70				75						80	
	Arg	Phe	Trp	Gly	Asp	Leu	Phe	Gly	Ala	Phe	Leu	Gly	Gly	Val	Cys	Gln	
					85					90					95		
20	Gly	Phe	Ser	Ser	Ser	Trp	Trp	Lys	Asp	Lys	His	Asn	Thr	His	His	Ala	
				100					105					110			
	Ala	Pro	Asn	Val	His	Gly	Glu	Asp	Pro	Asp	Ile	Asp	Thr	His	Pro	Leu	
25				115				120					125				
	Leu	Thr	Trp	Ser	Glu	His	Ala	Leu	Glu	Met	Phe	Ser	Asp	Val	Pro	Asp	
		130					135					140					
	Glu	Glu	Leu	Thr	Arg	Met	Trp	Ser	Arg	Phe	Met	Val	Leu	Asn	Gln	Thr	
30	145					150				155						160	
	Trp	Phe	Tyr	Phe	Pro	Ile	Leu	Ser	Phe	Ala	Arg	Leu	Ser	Trp	Cys	Leu	
					165					170					175		
35	Gln	Ser	Ile	Leu	Phe	Val	Leu	Pro	Asn	Gly	Gln	Ala	His	Lys	Pro	Ser	
				180					185					190			
	Gly	Ala	Arg	Val	Pro	Ile	Ser	Leu	Val	Glu	Gln	Leu	Ser	Leu	Ala	Met	
			195					200					205				
40	His	Trp	Thr	Trp	Tyr	Leu	Ala	Thr	Met	Phe	Leu	Phe	Ile	Lys	Asp	Pro	
		210					215					220					
	Val	Asn	Met	Leu	Val	Tyr	Phe	Leu	Val	Ser	Gln	Ala	Val	Cys	Gly	Asn	
45	225					230				235						240	
	Leu	Leu	Ala	Ile	Val	Phe	Ser	Leu	Asn	His	Asn	Gly	Met	Pro	Val	Ile	
				245						250				255			
50	Ser	Lys	Glu	Glu	Ala	Val	Asp	Met	Asp	Phe	Phe	Thr	Lys	Gln	Ile	Ile	
				260					265					270			
	Thr	Gly	Arg	Asp	Val	His	Pro	Gly	Leu	Phe	Ala	Asn	Trp	Phe	Thr	Gly	
			275					280					285				
55	Gly	Leu	Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Ser	Met	Pro	Arg	
		290					295					300					
	His	Asn	Phe	Ser	Lys	Ile	Gln	Pro	Ala	Val	Glu	Thr	Leu	Cys	Lys	Lys	
60	305					310				315						320	
	Tyr	Asn	Val	Arg	Tyr	His	Thr	Thr	Gly	Met	Ile	Glu	Gly	Thr	Ala	Glu	
					325					330					335		
65	Val	Phe	Ser	Arg	Leu	Asn	Glu	Val	Ser	Lys	Ala	Ala	Ser	Lys	Met	Gly	

340

345

350

Lys Ala Gln
355

5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
1 5 10 15

25

Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
20 25 30

30

Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
35 40 45

35

Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
50 55 60

Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
65 70 75 80

Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
85 90 95

40

Gly Pro Asn Leu Gln His Ile Pro
100

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 252 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln
1 5 10 15

60

Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile
20 25 30

65

Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn
35 40 45

5 Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
 65 70 75 80
 Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
 85 90 95
 Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
 10 100 105 110
 Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
 115 120 125

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30 Pro Ala Thr Glu Val Gly Gly Leu Ala Trp Met Ile Thr Phe Tyr Val
 1 5 10 15
 Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
 20 25 30
 35 Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
 35 40 45
 Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
 50 55 60
 40 Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
 65 70 75 80
 45 Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
 85 90 95
 His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110
 50 Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125
 Lys Pro Leu
 130

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys	Ser	Pro	Lys	Ser	Ser	Pro	Thr	Arg	Asn	Met	Thr	Pro	Ser	Pro	Phe
1				5					10					15	
Ile	Asp	Trp	Leu	Trp	Gly	Gly	Leu	Asn	Tyr	Gln	Ile	Glu	His	His	Leu
			20					25					30		
Phe	Pro	Thr	Met	Pro	Arg	Cys	Asn	Leu	Asn	Arg	Cys	Met	Lys	Tyr	Val
			35				40					45			
Lys	Glu	Trp	Cys	Ala	Glu	Asn	Asn	Leu	Pro	Tyr	Leu	Val	Asp	Asp	Tyr
	50					55					60				
Phe	Val	Gly	Tyr	Asn	Leu	Asn	Leu	Gln	Gln	Leu	Lys	Asn	Met	Ala	Glu
65					70					75					80
Leu	Val	Gln	Ala	Lys	Ala	Ala									
					85										

25 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg	His	Glu	Ala	Ala	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Tyr	Met	Leu	Val
1				5					10					15	
Cys	Met	Gln	Trp	Thr	Asp	Leu	Leu	Trp	Ala	Ala	Ser	Phe	Tyr	Ser	Arg
			20					25					30		
Phe	Phe	Leu	Ser	Tyr	Ser	Pro	Phe	Tyr	Gly	Ala	Thr	Gly	Thr	Leu	Leu
		35					40					45			
Leu	Phe	Val	Ala	Val	Arg	Val	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Ile
	50					55					60				
Thr	Gln	Met	Asn	His	Ile	Pro	Lys	Glu	Ile	Gly	His	Glu	Lys	His	Arg
65					70					75					80
Asp	Trp	Ala	Ser	Ser	Gln	Leu	Ala	Ala	Thr	Cys	Asn	Val	Glu	Pro	Ser
				85					90					95	
Leu	Phe	Ile	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His
			100					105					110		
His	Leu	Phe	Pro	Thr	Met	Thr	Arg	His	Asn	Tyr	Arg	Xaa	Val	Ala	Pro
		115					120					125			
Leu	Val	Lys	Ala	Phe	Cys	Ala	Lys	His	Gly	Leu	His	Tyr	Glu	Val	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCAAGCTTCT GCAGGAGCTC TTTTTTTTTT TTTT

35

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AACTGATCTA GATTACTTCT TGAAAAGAC CACGTCTCC

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 746 nucleic acids
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5	CGTATGTCAC	TCCATTCCAA	ACTCGTTCAT	GGTATCATAA	ATATCAACAC	ATTTACGCTC	60
	CACTCCTCTA	TGGTATTTAC	ACACTCAAAT	ATCGTACTCA	AGATTGGGAA	GCTTTTGTA	120
	AGGATGGTAA	AAATGGTGCA	ATTCGTGTTA	GTGTCGCCAC	AAATTTTCGAT	AAGGCCGCTT	180
	ACGTCATTGG	TAAATTGTCT	TTTGTTTTCT	TCCGTTTCAT	CCTTCCACTC	CGTTATCATA	240
	GCTTTACAGA	TTTAATTTGT	TATTCCTCA	TTGCTGAATT	CGTCTTTGGT	TGGTATCTCA	300
	CAATTAATTT	CCAAGTTAGT	CATGTCGCTG	AAGATCTCAA	ATTCTTTGCT	ACCCCTGAAA	360
10	GACCAGATGA	ACCATCTCAA	ATCAATGAAG	ATTGGGCAAT	CCTTCAACTT	AAAACACTC	420
	AAGATTATGG	TCATGGTTCA	CTCCTTTGTA	CCTTTTTCAG	TGGTTCTTTA	AATCATCAAG	480
	TTGTTTCATCA	TTTATTCCCA	TCAATTGCTC	AAGATTTCCTA	CCCACAACTT	GTACCAATTG	540
	TAAAAGAAGT	TTGTAAAGAA	CATAACATTA	CTTACCACAT	TAAACCAAAC	TTCACCTGAAG	600
	CTATTATGTC	ACACATTAAT	TACCTTTACA	AAATGGGTAA	TGATCCAGAT	TATGTTAAAA	660
15	AACCATTAGC	CTCAAAAGAT	GATTAAATGA	AATAACTTAA	AAACCAATTA	TTTACTTTTG	720
	ACAAACAGTA	ATATTAATAA	ATACAA				746

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30	Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln	1	5	10	15
	His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr	20	25	30	
35	Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly	35	40	45	
	Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr	50	55	60	
	Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro	65	70	75	
40	Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile	80	85	90	
	Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val	95	100	105	
45	Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg	110	115	120	
	Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln	125	130	135	
	Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr	140	145	150	
50	Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe	155	160	165	
	Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val	170	175	180	
55	Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro	185	190	195	
	Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys	200	205	210	
	Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys	215	220	225	
60	Asp Asp Xaa				

(2) INFORMATION FOR SEQ ID NO 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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TTTTGGAAGG	NTCCAAGTTN	ACCACGGANT	NGGCAAGTTN	ACGGGGCGGA	AANCGGTTTT	60
CCCCCAAGC	CTTTTGTGCA	CTGGTTCTGT	GGTGGCTTCC	AGTACCAAGT	CGACCACCAC	120
TTATTCCTCA	GCCTGCCCGG	ACACAATCTG	GCCAAGACAC	ACGCACTGGT	CGAATCGTTC	180
TGCAAGGAGT	GGGGTGTCCA	GTACCACGAA	GCCGACCTCG	TGGACGGGAC	CATGGAAGTC	240
TTGCACCATT	TGGGCAGCGT	GGCCGGCGAA	TTCGTCGTGG	ATTTTGTACG	CGACGGACCC	300
GCCATGTAAT	CGTCGTTCGT	GACGATGCAA	GGGTTACGCG	ACATCTACAC	ACACTCACTC	360
ACACAACCTAG	TGTAACCTCGT	ATAGAATTCG	GTGTCGACCT	GGACCTTGTT	TGACTGGTTG	420
GGGATAGGGT	AGGTAGGCGG	ACGCGTGGGT	CGNCCCCGGG	AATTCTGTGA	CCGGTACCTG	480
GGCCGCGTNA	AAGT					494

(2) INFORMATION FOR SEQ ID NO:22:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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Phe	Trp	Lys	Xaa	Pro	Ser	Xaa	Pro	Arg	Xaa	Xaa	Gln	Val	Xaa	Gly
1				5					10					15
Ala	Glu	Xaa	Gly	Phe	Pro	Pro	Lys	Pro	Phe	Val	Asp	Trp	Phe	Cys
				20					25					30
Gly	Gly	Phe	Gln	Tyr	Gln	Val	Asp	His	His	Leu	Phe	Pro	Ser	Leu
				35					40					45
Pro	Arg	His	Asn	Leu	Ala	Lys	Thr	His	Ala	Leu	Val	Glu	Ser	Phe
				50					55					60
Cys	Lys	Glu	Trp	Gly	Val	Gln	Tyr	His	Glu	Ala	Asp	Leu	Val	Asp
				65					70					75
Gly	Thr	Met	Glu	Val	Leu	His	His	Leu	Gly	Ser	Val	Ala	Gly	Glu
				65					70					75
Phe	Val	Val	Asp	Phe	Val	Arg	Asp	Gly	Pro	Ala	Met			
				80					85					

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 nucleic acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

5 GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTTAAGCGT CATGGGTGCG 60
 CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC 120
 ATTTACATT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG 180
 GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT 240
 GGT TTGTAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCA 300
 CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC 360
 10 ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC 420
 TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC 480
 TTAATTCCTCC ACCCCACCCC ATGTTCTGTC TTCCTCCCGC 520

15 (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

30 Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys
 1 5 10 15
 Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His
 20 25 30
 Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala
 35 40 45
 Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly
 50 55 60
 Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile
 65 70 75
 Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn
 80 85 90
 Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg
 95 100 105
 Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His
 110 115 120
 Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr
 125 130 135
 45 Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala
 140 145 150
 Lys Arg Asp

50 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 nucleic acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

65 ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC 60
 GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCTTTTG 120

5 GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC 180
 TCAGGGTCGC TGCGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTTCA CTGGTGTCTAT 240
 TTGGCTTGAC GACCGGTTGT GCGAGTTCTT TTACGGCGTT GGTGTGGCA TGAGCGGTCA 300
 TTAAGTGGAAA AACCAGCACA GCAAACACCA CGCAGCGCCA AACCAGGCTCG AGCAGCATGT 360
 AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC 420

10 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly
 1 5 10 15
 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu
 20 25 30
 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser
 35 40 45
 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser
 50 55 60
 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser
 65 70 75
 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe
 80 85 90
 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln
 95 100 105
 His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val
 110 115 120
 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val
 125
 Arg Lys Val Arg Pro

45 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA 60
 ACCTGATCCC AATTTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT 120
 TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCAATTTT GGGGCCTATG CGTTTGGCAG 180
 TTGCATTAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCACAATG CTGCCTTTGG 240
 CAACTGCAAA GCAATGTGGA ATCCTGTTT TGGAAATGTTT GCTAATCTTC CTATTGGGAT 300

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TCCATATTCA	ATTCCTTTA	AGAGGTATCA	CATGGATCAT	CATCGGTACC	TTGGAGCTGA	360
TGGCGTCGAT	GTAGATATTC	CTACCGATTT	TGAGGGCTGG	TTCTTCTGTA	CCGCTTTCAG	420
AAAGTTTATA	TGGGTATTC	TTCAGCCTCT	CTTTTATGCC	TTTCGACCTC	TGTTTCATCAA	480
CCCCAAACCA	ATTACGTATC	TGGAAGTTAT	CAATACCGTG	GCACAGGTCA	CTTTTGACAT	540
TTTAATTTAT	TACTTTTGG	GAATTAAATC	CTTAGTCTAC	ATGTTGGCAG	CATCTTTACT	600
TGGCCTGGGT	TTGCACCCAA	TTTCTGGACA	TTTTATAGCT	GAGCATTACA	TGTTCTTAAA	660
GGGTCATGAA	ACTTACTCAT	ATTATGGGCC	TCTGAATTTA	CTTACCTTCA	ATGTGGGTTA	720
TCATAATGAA	CATCATGATT	TCCCCAACAT	TCCTGGAAAA	AGTCTTCCAC	TGGTGAGGAA	780
AATAGCAGCT	GAATACTATG	ACAACCTCCC	TCACTACAAT	TCCTGGATAA	AAGTACTGTA	840
TGATTTTGTG	ATGGATGATA	CAATAAGTCC	CTACTCAAGA	ATGAAGAGGC	ACCAAAAAGG	900
AGAGATGGTG	CTGGAGTAAA	TATCATTAGT	GCCAAAGGGA	TTCTTCTCCA	AAACTTTAGA	960
TGATAAAATG	GAATTTTGC	ATTATTAAAC	TTGAGACCAG	TGATGCTCAG	AAGCTCCCCT	1020
GGCACAATTT	CAGAGTAAGA	GCTCGGTGAT	ACCAAGAAGT	GAATCTGGCT	TTTAAACAGT	1080
CAGCCTGACT	CTGTACTGCT	CAGTTTCACT	CACAGGAAAC	TTGTGACTTG	TGTATTATCG	1140
TCATTGAGGA	TGTTTCACTC	ATGTCTGTCA	TTTTATAAGC	ATATCATTTA	AAAAGCTTCT	1200
AAAAAGCTAT	TTCGCCAGG					1219

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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TTACCTTCTA	CGTCCGCTTC	TTCCTCACTT	ATGTGCCACT	ATTGGGGCTG	AAAGCTTCCT	60
GGGCCTTTTC	TTCATAGTCA	GGTTCCTGGA	AAGCAACTGG	TTTGTGTGGG	TGACACAGAT	120
GAACCATATT	CCCATGCACA	TTGATCATGA	CCGGAACATG	GACTGGGTTT	CCACCCAGCT	180
CCAGGCCACA	TGCAATGTCC	ACAAGTCTGC	CTTCAATGAC	TGGTTCAGTG	GACACCTCAA	240
CTTCCAGATT	GAGCACCATC	TTTTTCCCAC	GATGCCTCGA	CACAATTACC	ACAAAGTGGC	300
TCCCCTGGTG	CAGTCCTTGT	GTGCCAAGCA	TGGCATAGAG	TACCAGTCCA	AGCCCCTGCT	360
GTCAGCCTTC	GCCGACATCA	TCCACTCACT	AAAGGAGTCA	GGGCAGCTCT	GGCTAGATGC	420
CTATCTTCAC	CAATAACAAC	AGCCACCCTG	CCCAGTCTGG	AAGAAGAGGA	GGAAGACTCT	480
GGAGCCAAGG	CAGAGGGGAG	CTTGAGGGAC	AATGCCACTA	TAGTTTAATA	CTCAGAGGGG	540

GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA 600
 GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT 655

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCTTTTACT TTGGCAATGG CTGGATTCTT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60
 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
 CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
 AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
 CCCGATGTGA ACATGCTGCA CGTGTTTGTG CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
 AAGA 304

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 918 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC 420
 TTTGGGACGT CCTTTTGGC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC 480
 CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG 540
 AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG 600
 AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC 660

AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG 720
 AAGAAAAAAT ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA 780
 5 GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG 840
 TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC 900
 10 ACCGCAAATG CTTCTAAA 918

(2) INFORMATION FOR SEQ ID NO:31:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

25 GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA 60
 AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGGCG 120
 30 AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAGC 180
 ACGAATACTT CTTCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTT CAGTACCAGA 240
 TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT 300
 35 ACATCCGGTT CTTTCATCACC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTTCC 360
 TCAACTTCAT CAGGTTCCCTG GAGAGCCACT GGTTCGTGTG GTTCACACAG ATGAATCACA 420
 40 TCGTCATGGA GATTGACCAG GAGGCCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA 480
 CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGGACACCTT AACTTCCAGA 540
 TTGAGACCA CCTCTTCCCC ACCATGCCCC GGCACAACCT ACACAAGATC GCCCCGCTGG 600
 45 TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC 660
 TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC 720
 50 ACAAATGAAG CCACAGCCCC CGGGACACCG TGGGAAGGG GTGCAGGTGG GGTGATGGCC 780
 AGAGGAATGA TGGGCTTTTG TTCTGAGGGG TGTCAGAGAG GCTGGTGTAT GCACTGCTCA 840
 CGGACCCCAT GTTGGATCTT TCTCCCTTTT TCCTCTCCTT TTTCTCTTCA CATCTCCCCC 900
 55 ATAGCACCCT GCCCTCATGG GACCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC 960
 TCCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC 1020
 60 TGTCCTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGAGA CCAGCGGTCC ATGGGTCTGG 1080
 CCTGTGAGTC TCCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCCTTTG GTTCTTCAGA 1140
 TGCTCTTGGG GTTCATAGGG GCAGGTCCTA GTCGGGCAGG GCCCCTGACC CTCCCGGCCT 1200
 65 GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCTTT CATAGAGAGG CCTGCTTTGT 1260

5 TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTAAAGTAC CCGAGGCCTC TCTTAAGATG 1320
TCCAGGGCCC CAGGCCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC 1380
CACCCTATCA CTAGAGTGCT CTGACCCTGG GCTTTCACGG GCCCCATTCC ACCGCCTCCC 1440
CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGA CT CAGCA 1500
10 GAGGCAGTGG CCACGTT CAG GGAGGGGCCG GCTGGCCTGG AGGCTCAGCC CACCCTCCAG 1560
CTTTTCCTCA GGGTGTCTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCT TCTCCAAAGG 1620
15 CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG 1680
GCCCTG 1686

20 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1843 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (Contig 2535)
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60
35 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
40 CCCGATGTGA ACATGCTGCA CGTGTTTGT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG 360
45 CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT 420
AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTTCTT CATCACCTAC 480
ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTTCCTCA ACTTCATCAG GTTCCTGGAG 540
50 AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG 600
GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC 660
TTCAACGACT GGTTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC 720
55 ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT 780
GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG 840
60 AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG 900
GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTT 960
65 TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCATGTT GGATCTTTCT 1020

5 CCCTTTCTCC TCTCCTTTTT CTCTTCACAT CTCCCCATA GCACCCTGCC CTCATGGGAC 1080
 CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCCTTC 1140
 TTCCAAGGAG CAGAGAGGTG GCCACCGGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC 1200
 CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CTTGCAGCC 1260
 10 TGGTCACTAG GCATCACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA 1320
 GGTCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG 1380
 CCATTGGTCC ACCCTTTTCAT AGAGAGGCCT GCTTTGTAC AAAGCTCGGG TCTCCCTCCT 1440
 15 GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCGCGGGC 1500
 ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCTCCAC CCCATCACTA GAGTGCTCTG 1560
 ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG 1620
 20 ACCAAAGGGG GAGTCCCTCG TCTCTTGTGA CTCAGCAGAG GCAGTGGCCA CGTTCAGGGA 1680
 GGGGCCGGCT GGCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCTCAGGG TGTCTGAGG 1740
 25 TCCAAGATTC TGGAGCAATC TGACCCTTCT CCAAAGGCTC TGTATCAGC TGGGCAGTGC 1800
 CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG 1843

30 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2257 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 45 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CTTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 50 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGAG CCTGGCTCAC CTTTGGGTC 420
 55 TTTGGGACGT CCTTTTGGCC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGCAG 480
 GCCCAAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG 540
 60 TGGAACCACC TTGTCCACAA ATTCGTCATT GGCCACTTAA AGGGTGCCTC TGCCAACTGG 600
 TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCCACAA GGATCCCGAT 660
 65 GTGAACATGC TGCACGTGTT TGTTCTGGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG 720

5 AAGCTGAAAT ACCTGCCCTA CAATCACCAG CACGAATACT TCTTCCTGAT TGGGCCGCCG 780
 CTGCTCATCC CCATGTATTT CCAGTACCAG ATCATCATGA CCATGATCGT CCATAAGAAC 840
 10 TGGGTGGACC TGGCCTGGGC CGTCAGCTAC TACATCCGGT TCTTCATCAC CTACATCCCT 900
 TTCTACGGCA TCCTGGGAGC CCTCCTTTTC CTCAACTTCA TCAGGTTCCCT GGAGAGCCAC 960
 TGGTTTGTGT GGGTCACACA GATGAATCAC ATCGTCATGG AGATTGACCA GGAGGCCTAC 1020
 15 CGTGACTGGT TCAGTAGCCA GCTGACAGCC ACCTGCAACG TGGAGCAGTC CTTCTTCAAC 1080
 GACTGGTTCA GTGGACACCT TAACTTCCAG ATTGAGCACC ACCTCTTCCC CACCATGCCC 1140
 CGGCACAACT TACACAAGAT CGCCCCGCTG GTGAAGTCTC TATGTGCCAA GCATGGCATT 1200
 20 GAATACCAGG AGAAGCCGCT ACTGAGGGCC CTGCTGGACA TCATCAGGTC CCTGAAGAAG 1260
 TCTGGGAAGC TGTGGCTGGA CGCCTACCTT CACAAATGAA GCCACAGCCC CCGGGACACC 1320
 GTGGGGAAGG GGTGCAGGTG GGGTGATGGC CAGAGGAATG ATGGGCTTTT GTTCTGAGGG 1380
 25 GTGTCCGAGA GGCTGGTGTA TGCACTGCTC ACGGACCCCA TGTGGATCT TTCTCCCTTT 1440
 CTCCTCTCCT TTTTCTCTC ACATCTCCCC CATAGCACCC TGCCCTCATG GGACCTGCCC 1500
 TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCTAGCCC CTTCTTCCAA 1560
 30 GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGTCCTACC TCCACTCTCT GCCCCTAAAG 1620
 ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA 1680
 CTAGGCATCA CCCCCGCTTT GGTTCTTCAG ATGCTCTTGG GGTTCATAGG GGCAGGTCCT 1740
 35 AGTCGGGCAG GGCCCTGAC CCTCCCGGCC TGGCTTCACT CTCCTGACG GCTGCCATTG 1800
 GTCCACCCTT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT 1860
 40 CGGTTAAGTA CCCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCGC GGGCACAGCC 1920
 AGCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCCTG 1980
 GGCTTTACAG GGCCCCATTC CACCGCTCC CCAACTTGAG CCTGTGACCT TGGGACCAAA 2040
 45 GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGGCC 2100
 GGCTGGCCTG GAGGCTCAGC CCACCCTCCA GCTTTTCCTC AGGGTGTCTT GAGGTCCAAG 2160
 50 ATTCTGGAGC AATCTGACCC TTCTCAAAG GCTCTGTTAT CAGCTGGGCA GTGCCAGCCA 2220
 ATCCCTGGCC ATTTGGCCCC AGGGGACGTG GGCCCTG 2257

55 (2) INFORMATION FOR SEQ ID NO:34:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

	His	Ala	Asp	Arg	Arg	Arg	Glu	Ile	Leu	Ala	Lys	Tyr	Pro	Glu	Ile	
	1				5					10					15	
5	Lys	Ser	Leu	Met	Lys	Pro	Asp	Pro	Asn	Leu	Ile	Trp	Ile	Ile	Ile	
					20					25					30	
	Met	Met	Val	Leu	Thr	Gln	Leu	Gly	Ala	Phe	Tyr	Ile	Val	Lys	Asp	
					35					40					45	
	Leu	Asp	Trp	Lys	Trp	Val	Ile	Phe	Gly	Ala	Tyr	Ala	Phe	Gly	Ser	
					50					55					60	
10	Cys	Ile	Asn	His	Ser	Met	Thr	Leu	Ala	Ile	His	Glu	Ile	Ala	His	
					65					70					75	
	Asn	Ala	Ala	Phe	Gly	Asn	Cys	Lys	Ala	Met	Trp	Asn	Arg	Trp	Phe	
					80					85					90	
15	Gly	Met	Phe	Ala	Asn	Leu	Pro	Ile	Gly	Ile	Pro	Tyr	Ser	Ile	Ser	
					95					100					105	
	Phe	Lys	Arg	Tyr	His	Met	Asp	His	His	Arg	Tyr	Leu	Gly	Ala	Asp	
					110					115					120	
	Gly	Val	Asp	Val	Asp	Ile	Pro	Thr	Asp	Phe	Glu	Gly	Trp	Phe	Phe	
					125					130					135	
20	Cys	Thr	Ala	Phe	Arg	Lys	Phe	Ile	Trp	Val	Ile	Leu	Gln	Pro	Leu	
					140					145					150	
	Phe	Tyr	Ala	Phe	Arg	Pro	Leu	Phe	Ile	Asn	Pro	Lys	Pro	Ile	Thr	
					155					160					165	
25	Tyr	Leu	Glu	Val	Ile	Asn	Thr	Val	Ala	Gln	Val	Thr	Phe	Asp	Ile	
					170					175					180	
	Leu	Ile	Tyr	Tyr	Phe	Leu	Gly	Ile	Lys	Ser	Leu	Val	Tyr	Met	Leu	
					185					190					195	
	Ala	Ala	Ser	Leu	Leu	Gly	Leu	Gly	Leu	His	Pro	Ile	Ser	Gly	His	
					200					205					210	
30	Phe	Ile	Ala	Glu	His	Tyr	Met	Phe	Leu	Lys	Gly	His	Glu	Thr	Tyr	
					215					220					225	
	Ser	Tyr	Tyr	Gly	Pro	Leu	Asn	Leu	Leu	Thr	Phe	Asn	Val	Gly	Tyr	
					230					235					240	
35	His	Asn	Glu	His	His	Asp	Phe	Pro	Asn	Ile	Pro	Gly	Lys	Ser	Leu	
					245					250					255	
	Pro	Leu	Val	Arg	Lys	Ile	Ala	Ala	Glu	Tyr	Tyr	Asp	Asn	Leu	Pro	
					260					265					270	
	His	Tyr	Asn	Ser	Trp	Ile	Lys	Val	Leu	Tyr	Asp	Phe	Val	Met	Asp	
					275					280					285	
40	Asp	Thr	Ile	Ser	Pro	Tyr	Ser	Arg	Met	Lys	Arg	His	Gln	Lys	Gly	
					290					295					300	
	Glu	Met	Val	Leu	Glu	Xaa	Ile	Ser	Leu	Val	Pro	Lys	Gly	Phe	Phe	
					305					310					315	
45	Ser	Lys	Thr	Leu	Asp	Asp	Lys	Met	Glu	Phe	Leu	His	Tyr	Xaa	Thr	
					320					325					330	
	Xaa	Asp	Gln	Xaa	Cys	Ser	Glu	Ala	Pro	Leu	Ala	Gln	Phe	Gln	Ser	
					335					340					345	
	Lys	Ser	Ser	Val	Ile	Pro	Arg	Ser	Glu	Ser	Gly	Phe	Xaa	Thr	Val	
					350					355					360	
50	Ser	Leu	Thr	Leu	Tyr	Cys	Ser	Val	Ser	Leu	Thr	Gly	Asn	Leu	Xaa	
					365					370					375	
	Leu	Val	Tyr	Tyr	Arg	His	Xaa	Gly	Cys	Phe	Thr	His	Val	Cys	His	
					380					385					390	
55	Phe	Ile	Ser	Ile	Ser	Phe	Lys	Lys	Leu	Leu	Lys	Ser	Tyr	Phe	Ala	
					400					405					410	
	Arg															

(2) INFORMATION FOR SEQ ID NO:35:

- 60 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 65

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

5
Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly
1 5 10 15
Ala Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu
20 25 30
10 Ser Asn Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met
35 40 45
His Ile Asp His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu
50 55 60
15 Gln Ala Thr Cys Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe
65 70 75
Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
80 85 90
Met Pro Arg His Asn Tyr His Lys Val Ala Pro Leu Val Gln Ser
95 100 105
20 Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser Lys Pro Leu Leu
110 115 120
Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu Ser Gly Gln
125 130 135
25 Leu Trp Leu Asp Ala Tyr Leu His Gln Xaa Gln Gln Pro Pro Cys
140 145 150
Pro Val Trp Lys Lys Arg Arg Lys Thr Leu Glu Pro Arg Gln Arg
155 160 165
Gly Ala Xaa Gly Thr Met Pro Leu Xaa Phe Asn Thr Gln Arg Gly
170 175 180
30 Leu Gly Leu Gly Thr Xaa Ser Leu Xaa Leu Lys Leu Leu Pro Phe
185 190 195
Ile Phe Xaa Pro Gln Phe Xaa Asp Pro Lys Trp Gly Val Asp Thr
200 205 210
35 Glu Val Pro Arg Arg Glu Gly Ala
215

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

50
Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
1 5 10 15
55 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
20 25 30
Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
35 40 45
60 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
50 55 60
Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
65 70 75
Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xaa
80 85

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
1 5 10 15
Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
20 25 30
Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
35 40 45
Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
50 55 60
Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
25 65 70 75
Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
80 85 90
Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
95 100 105
30 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
110 115 120
Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
125 130 135
Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
35 140 145 150
Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu
155 160 165
Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
170 175 180
40 Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala
185 190 195
Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys
200 205 210
Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe
45 215 220 225
Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
230 235 240
Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xaa Tyr Phe Phe
245 250 255
50 Leu Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr
260 265 270
Ile Phe Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala
275 280 285
Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser
55 290 295 300
Thr Ala Asn Ala Ser Lys
305

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 566 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	His	Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	
	1				5					10					15	
10	Gln	His	His	Ala	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	
					20					25					30	
	Asn	Met	Leu	His	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	
					35					40					45	
15	Tyr	Gly	Lys	Lys	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	
					50					55					60	
	Glu	Tyr	Phe	Phe	Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	
					65					70					75	
	Phe	Gln	Tyr	Gln	Ile	Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp	
					80					85					90	
20	Val	Asp	Leu	Ala	Trp	Ala	Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	
					95					100					105	
	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	
					110					115					120	
25	Asn	Phe	Ile	Arg	Phe	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Val	Thr	
					125					130					135	
	Gln	Met	Asn	His	Ile	Val	Met	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	
					140					145					150	
	Asp	Trp	Phe	Ser	Ser	Gln	Leu	Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	
					155					160					165	
30	Ser	Phe	Phe	Asn	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	
					170					175					180	
	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	His	Lys	
					185					190					195	
35	Ile	Ala	Pro	Leu	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	
					200					205					210	
	Tyr	Gln	Glu	Lys	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	
					215					220					225	
	Ser	Leu	Lys	Lys	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	
					230					235					240	
40	Lys	Xaa	Ser	His	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	
					245					250					255	
	Trp	Gly	Asp	Gly	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	Xaa	Gly	Val	
					260					265					270	
45	Ser	Glu	Arg	Leu	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	
					275					280					285	
	Leu	Ser	Pro	Phe	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His	Leu	Pro	His	
					290					295					300	
	Ser	Thr	Leu	Pro	Ser	Trp	Asp	Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro	
					305					310					315	
50	Ser	Ala	Met	Ala	Leu	Pro	Val	Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly	
					320					325					330	
	Ala	Glu	Arg	Trp	Pro	Pro	Gly	Val	Ala	Leu	Ser	Tyr	Leu	His	Ser	
					335					340					345	
	Leu	Pro	Leu	Lys	Met	Gly	Gly	Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala	
55					350					355					360	
	Cys	Glu	Ser	Pro	Leu	Ala	Ala	Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala	
					365					370					375	
	Leu	Val	Leu	Gln	Met	Leu	Leu	Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser	
					380					385					390	
60	Arg	Ala	Gly	Pro	Leu	Thr	Leu	Pro	Ala	Trp	Leu	His	Ser	Pro	Xaa	
					400					405					410	
	Arg	Leu	Pro	Leu	Val	His	Pro	Phe	Ile	Glu	Arg	Pro	Ala	Leu	Leu	
					415					420					425	
65	Gln	Ser	Ser	Gly	Leu	Pro	Pro	Ala	Ala	Arg	Leu	Ser	Thr	Arg	Gly	
					430					435					440	

5 Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser
 445 450 455
 Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser
 460 465 470
 Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
 475 480 485
 Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu
 490 495 500
 10 Leu Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly
 505 510 515
 Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val
 520 525 530
 Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala
 535 540 545
 15 Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
 550 555 560
 Pro Gly Asp Val Gly Pro Xaa
 565

20

(2) INFORMATION FOR SEQ ID NO:39:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

35 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
 1 5 10 15
 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
 20 25 30
 40 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
 35 40 45
 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
 50 55 60
 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
 65 70 75
 45 Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val
 80 85 90
 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys
 95 100 105
 50 Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly
 110 115 120
 Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met
 125 130 135
 Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val
 140 145 150
 55 Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly
 155 160 165
 Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu
 170 175 180
 Ser His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met
 185 190 195
 60 Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu
 200 205 210
 Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe
 215 220 225
 65 Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr

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		230		235		240
	Met	Pro	Arg	His	Asn	Leu
					His	Lys
					Ile	Ala
					Pro	Leu
					Val	Lys
					Ser	
					245	255
	Leu	Cys	Ala	Lys	His	Gly
					Ile	Glu
					Tyr	Gln
					Glu	Lys
					Pro	Leu
					Leu	
					260	270
	Arg	Ala	Leu	Leu	Asp	Ile
					Ile	Arg
					Ser	Leu
					Lys	Lys
					Ser	Gly
					Lys	
					275	285
	Leu	Trp	Leu	Asp	Ala	Tyr
					Leu	His
					Lys	Xaa
					Ser	His
					Ser	Pro
					Arg	
					290	300
	Asp	Thr	Val	Gly	Lys	Gly
					Cys	Arg
					Trp	Gly
					Asp	Gly
					Gln	Arg
					Asn	
					305	315
	Asp	Gly	Leu	Leu	Phe	Xaa
					Gly	Val
					Ser	Glu
					Arg	Leu
					Val	Tyr
					Ala	
					320	330
	Leu	Leu	Thr	Asp	Pro	Met
					Leu	Asp
					Leu	Ser
					Pro	Phe
					Leu	Leu
					Ser	
					335	345
	Phe	Phe	Ser	Ser	His	Leu
					Pro	His
					Ser	Thr
					Leu	Pro
					Ser	Trp
					Asp	
					350	360
	Leu	Pro	Ser	Leu	Ser	Arg
					Gln	Pro
					Ser	Ala
					Met	Ala
					Leu	Pro
					Val	
					365	375
	Pro	Pro	Ser	Pro	Phe	Phe
					Gln	Gly
					Ala	Glu
					Arg	Trp
					Pro	Pro
					Gly	
					380	390
	Val	Ala	Leu	Ser	Tyr	Leu
					His	Ser
					Leu	Pro
					Leu	Lys
					Met	Gly
					Gly	
					400	410
	Asp	Gln	Arg	Ser	Met	Gly
					Leu	Ala
					Cys	Glu
					Ser	Pro
					Leu	Ala
					Ala	
					415	425
	Trp	Ser	Leu	Gly	Ile	Thr
					Pro	Ala
					Leu	Val
					Leu	Gln
					Met	Leu
					Leu	
					430	440
	Gly	Phe	Ile	Gly	Ala	Gly
					Pro	Ser
					Arg	Ala
					Gly	Pro
					Leu	Thr
					Leu	
					445	455
	Pro	Ala	Trp	Leu	His	Ser
					Pro	Xaa
					Arg	Leu
					Pro	Leu
					Val	His
					Pro	
					460	470
	Phe	Ile	Glu	Arg	Pro	Ala
					Leu	Leu
					Gln	Ser
					Ser	Gly
					Leu	Pro
					Pro	
					475	485
	Ala	Ala	Arg	Leu	Ser	Thr
					Arg	Gly
					Leu	Ser
					Xaa	Asp
					Val	Gln
					Gly	
					490	500
	Pro	Arg	Pro	Ala	Gly	Thr
					Ala	Ser
					Pro	Asn
					Leu	Gly
					Pro	Trp
					Lys	
					505	515
	Ser	Pro	Pro	Pro	His	His
					Xaa	Ser
					Ala	Leu
					Thr	Leu
					Gly	Phe
					His	
					520	530
	Gly	Pro	His	Ser	Thr	Ala
					Ser	Pro
					Thr	Xaa
					Ala	Cys
					Asp	Leu
					Gly	
					535	545
	Thr	Lys	Gly	Gly	Val	Pro
					Arg	Leu
					Leu	Xaa
					Leu	Ser
					Arg	Gly
					Ser	
					550	560
	Gly	His	Val	Gln	Gly	Gly
					Ala	Gly
					Trp	Pro
					Gly	Gly
					Ser	Ala
					His	
					565	575
	Pro	Pro	Ala	Phe	Pro	Gln
					Gly	Val
					Leu	Arg
					Ser	Lys
					Ile	Leu
					Glu	
					580	590
	Gln	Ser	Asp	Pro	Ser	Pro
					Lys	Ala
					Leu	Ser
					Ala	Gly
					Gln	Cys
					595	605
	Gln	Pro	Ile	Pro	Gly	His
					Leu	Ala
					Pro	Gly
					Asp	Val
					Gly	Pro
					Xaa	
					610	620

55

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

	Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln	1 5 10 15
5	Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val	20 25 30
	Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg	35 40 45
10	Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val	50 55 60
	Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser	65 70 75
	Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro	80 85 90
15	Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala	95 100 105
	Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe	110 115 120
20	Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp	125 130 135
	Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu	140 145 150
	Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp	155 160 165
25	Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys	170 175 180
	Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly	185 190 195
30	Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala	200 205 210
	Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His	215 220 225
	Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys	230 235 240
35	Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe	245 250 255
	Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln	260 265 270
40	Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala	275 280 285
	Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro	290 295 300
	Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg	305 310 315
45	Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His	320 325 330
	Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser	335 340 345
50	Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn	350 355 360
	Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu	365 370 375
	Phe Pro Thr Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu	380 385 390
55	Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys	400 405 410
	Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys	415 420 425
60	Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys Xaa Ser His	430 435 440
	Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly	445 450 455
	Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg Leu	460 465 470
65	Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe	

		475		480		485
	Leu Leu Ser Phe	Phe Ser Ser His Leu	Pro His Ser Thr Leu	Pro		
		490		495		500
5	Ser Trp Asp Leu	Pro Ser Leu Ser Arg	Gln Pro Ser Ala Met	Ala		
		505		510		515
	Leu Pro Val Pro	Pro Ser Pro Phe Phe	Gln Gly Ala Glu Arg	Trp		
		520		525		530
	Pro Pro Gly Val	Ala Leu Ser Tyr Leu	His Ser Leu Pro Leu	Lys		
		535		540		545
10	Met Gly Gly Asp	Gln Arg Ser Met Gly	Leu Ala Cys Glu Ser	Pro		
		550		555		560
	Leu Ala Ala Trp	Ser Leu Gly Ile Thr	Pro Ala Leu Val Leu	Gln		
		565		570		575
15	Met Leu Leu Gly	Phe Ile Gly Ala Gly	Pro Ser Arg Ala Gly	Pro		
		580		585		590
	Leu Thr Leu Pro	Ala Trp Leu His Ser	Pro Xaa Arg Leu Pro	Leu		
		595		600		605
	Val His Pro Phe	Ile Glu Arg Pro Ala	Leu Leu Gln Ser Ser	Gly		
		610		615		620
20	Leu Pro Pro Ala	Ala Arg Leu Ser Thr	Arg Gly Leu Ser Xaa	Asp		
		625		630		635
	Val Gln Gly Pro	Arg Pro Ala Gly Thr	Ala Ser Pro Asn Leu	Gly		
		640		645		650
25	Pro Trp Lys Ser	Pro Pro Pro His His	Xaa Ser Ala Leu Thr	Leu		
		655		660		665
	Gly Phe His Gly	Pro His Ser Thr Ala	Ser Pro Thr Xaa Ala	Cys		
		670		675		680
	Asp Leu Gly Thr	Lys Gly Gly Val Pro	Arg Leu Leu Xaa Leu	Ser		
		685		690		695
30	Arg Gly Ser Gly	His Val Gln Gly Gly	Ala Gly Trp Pro Gly	Gly		
		700		705		710
	Ser Ala His Pro	Pro Ala Phe Pro Gln	Gly Val Leu Arg Ser	Lys		
		715		720		725
35	Ile Leu Glu Gln	Ser Asp Pro Ser Pro	Lys Ala Leu Leu Ser	Ala		
		730		735		740
	Gly Gln Cys Gln	Pro Ile Pro Gly His	Leu Ala Pro Gly Asp	Val		
		745		750		755
	Gly Pro Xaa					